BX354591 602947063 AGENCOURT

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601589730

601334715 601513909 601564420

AL528496

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Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB E Maximum DB E

Database

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 719)

S NIH-MGC http://mgc.nci.nih.gov/

L Unpublished (1999)

L Unpublished (1999)

L Contact: Robert Strausberg, Ph.D.

Email: cgapba-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov

Plate: LLCM136 row: h column: 10

High quality sequence stop: 717.

Location/Qualifiers
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/mol_type="mRNA"
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BG751059 602729849
              AL52532 A
AL52192 A
AL52196 B
B1465298 G
AL518571 A
AA51871 A
AA55754 B
BE74882 B
AL557131 A
BX3575131 A
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                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                B1465298
AL518571
AW245754
BE784749
BX448882
AL557131
BX3545131
BX3545478
BX334776
BX328496
BX33172
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mRNA sequence.
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348
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                      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Score

Result No.

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Best Local Similarity 100.0%; P. Matches 348; Conservative 0;
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/tissue type="melanotic melanoma"
/tissue type="melanotic melanoma"
/tissue type="bild" the properties of the propert
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                                                              1 TTCGAGGCGGGCGGCCGCCGCCCCCTGGGGAAGAAGAAGACCTGTGTGCAGCATTT 60
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NIH-MGC http://mgc.nci.nih.gov/.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM36 row: h column: 01
High quality sequence stop: 733.
Location/Qualifiers
                                                                                                                                                                                                                                                196 AACGICATATGIGATAATGIGGGAAAGATTGGAGAAGGCTGGCTCGTCAGCTCAAAGTC
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   0; Mismatches
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Contect: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arcc/bCrD/DTP
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DB 2; Length 774;

100.0%; Score 348;

Query Match

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/issue type="adenocarcinoma, cell line"
/lab host="HINDB (phage-resistant)"
/lab host="HINDB (phage-resistant)"
/lone_lib="NIH_MGC_107"
/note="Organ: breast; Vector: pOTB7; Site_1: EcoR1;
Site_2: Xho1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/KhoI sites using the
following 5: dasperor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Strategne) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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AGENCOURT 10622000 NIH MGC 107 Homo sapiens cDNA clone
IMAGE:6731271 5', mRNA sequence.
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NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                           1 TTCGAGGCGGGGCGGCCGGCCGCCCTGGGGAAGAGACCTGTGTGCAGCATTT
                                 Gaps
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3057 row: g column: 14
High quality sequence stop: 650.
Location/Qualifiers
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                                 Indels
Pred. No. 1.2e-83;
Mismatches 0;
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/organism="Homo sapiens"
/mol_type="mRNN"
/db_xref="taxon:9606"
/clone="IMAGE:6731271"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 940)

E 1 (bases 1 to 940)

E 1 (bases 1 to 940)

I Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2460 row; p column: 15

High quality sequence stop; 488.
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AGENCOURT_8349344 NIH_MGC_102 Homo sapiens CDNA clone IMAGE:6276350
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                                                                                                                    Length 931;
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Note: this is a NIH_MGC Library."
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                                                                                                            Query Match
100.0%; Score 348; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.3e-83;
Matches 348; Conservative 0; Mismatches 0;
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Homo sapiens
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/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 107"
/note="Gorgan: breast, Vector: pOTB7; Site_1: EcoR1;
Site_2: Xho1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 93)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2740 row: h column: 01
High quality sequence stop: 506.
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AGENCOURT 10217577 NIH_MGC_107 Homo sapiens cDNA clone
IMAGE:6563185 5', mRNA sequence.
BU535532
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                                                      Length 850;
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                                             Match 100.0%; Score 348; DB 5; Local Similarity 100.0%; Pred. No. 1.2e-83; les 348; Conservative 0; Mismatches 0;
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/mol_type="mRNA"
/db xref="taxon:9606"
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Homo sapiens
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Matches 348
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AUTHORS
TITLE
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BU535532
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 947)

S NIH-MGC http://mgc.nci.nih.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov
Tissue Procurement: ArCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 575.

High quality sequence stop: 575.
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/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 102"
/note="Organ: salivary gland, Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI, coNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the
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947 bp mRNA linear EST 04-SEP-2002
AGENCOURT_8045256 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6086524
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(University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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                                                                                                                           Length 940;
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                                                                                                                      100.0%; Score 348; DB 5;
100.0%; Pred. No. 1.3e-83;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:6086524"
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Homo sapiens
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BU197303
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FEATURES

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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mommalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

11,W.B., Gruber,C., Jessee,J. and Polayes,D.

Pull-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31270330.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invirson of This sequence belongs to sequence cluster
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following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                             150 TTCGAGGCGGGGCGGCCGGGCCGCCCTGGGGAGAGAACACTGTGTGCAGCATTT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO14YN05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
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0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 348; Conservative 0
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1029 bp DNA linear GSS 15-DEC-2003
VIRTUAL TRANSCRIPT, partial sequence,
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1 (bases 1 to 1029)
1 (Lark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inferring nonneutral evolution from human-chimp-mouse orthologous
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.
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Location/Qualifiers
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Trodd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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Best Local Similarity 100.0%; Pred. No. 1.3e-83;
Matches 348; Conservative 0; Mismatches 0;
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AL527771
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/clone lib="Homo sapiens NBUROBLASTOMA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
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1 (bases 1 to 993)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
      /note="lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Matches 348; Conservative
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1. (Dases 1 to 1134)

2. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

3. Full-length cDNA libraries and normalization

3. Injw.B., Gruber, C., Jessee, J. and Polayes, D.

4. Unpublished (2001)

5. On Feb 15, 2001 this sequence version replaced gi:31266401.

6. Contact: Genoscope

7. The Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

8. Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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/note="list strand oDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                            Gaps
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                     Length 1029;
                                                            Indels
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                       ; Score 348; DB 9;
; Pred. No. 1.3e-83;
0; Mismatches 0;
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/db_xref="taxon:9606"
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                         100.0%;
100.0%;
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                         Query Match
Best Local Similarity 100.
Matches 348; Conservative
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AL544558
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Strand cDAA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length, CDNA libraries and normalization
                                                                                                                                                                                                  CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG
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     Length 1134;
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/db_xref="taxon:9606"
/clone="CSODJ011YK23"
/tissue_type="T_cells (Jurkat cell line)
10-normalized"
/plasmid="pCMVSPORT_6"
                                                 Indels
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Pred. No. 1.4e-83;
Score 348; DB 1;
Pred. No. 1.3e-83;
0; Mismatches 0;
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 BVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr

184 b: www.genoscope.cns.fr)
185 strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1614 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI067YD16 of Placenta Cot 25-normalized of Anono sapiens (human).
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                  241 GTGGGGGCTCTCAGGTCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTCAG
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                                                    CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 348; DB 3; Length 1614; 100.0%; Pred. No. 1.4e-83;
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/plasmid="pCMVSPORT_6"
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Mammalia; Butheria; Primates; Catarrhini; Hor
11 (bases 1 to 1614)
Li, W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length, CDNA libraries and normalization
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HTC; CNSLT CDNA.
Homo sapiens (human)
Homo sapiens
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Matches 348; Conservative
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
192 strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
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/tissue_type="HeLa cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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100.0%; Pred. No. 1.4e-83;
Live 0; Mismatches 0;
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             Mismatches
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 9100 GE DYR cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | 191 9100 GE DYR cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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T cells (Jurkat cell line)
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Catarrhini, Hominidae, Homo.
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            482 TCAGACACCAAGATCGACAGCATCGAGACAGATACCCCCGCAACCTGACAGAGCGTGTG
                                                                                                                          542 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCCAACAGTGGCCCACCTG
                                                                   181 CGGGAGTCACTGAGAATCTGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACCTG
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/tissue_type="T cells (Jurkat cell line)"
/plasmid="pCMVSPORT_6"
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100.0%; Pred. No. 1.4e-83;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates;
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HTC; CNSLT_cDNA.
Homo sapiens (human)
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Submitted (20-JUJ-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr.
Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecok V sites of the pCMVSpORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                             TCAGACACCAAGATCGACAACATCGAGGACAGATACCCCCGCAACCTGACAGGCGTGTG 180
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1 (bases 1 to 1618)
1 (M.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        full-length cDNA clone CS0DC019YA19 of Neuroblastoma Cot
25-normalized of Homo sapiens (human).
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//organism="Homo sapiens"
//organism="Homo sapiens"
//ol_type="mRMA"
/db_xref="taxon:9606"
/clone="CS0DCOL9YA19"
/tissue type="Neuroblastoma Cot 25-normalized"
/plasmid="pcMVSPORT_6"
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100.0%; Pred. No. 1.4e-83;
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Homo sapiens
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Best Local Similarity 100.
Matches 348; Conservative
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